

BLAST Basic Local Alignment Search Tool

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

SEQ ID NO:3 Fallon

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|25731

Description

None

Molecule type

nucleic acid

Query Length

633

Database Name

nr

Description

All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Program

BLASTN 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Database

Posted date	Nov 27, 2008 5:45 PM
Number of letters	251,403,974
Number of sequences	7,776,524
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

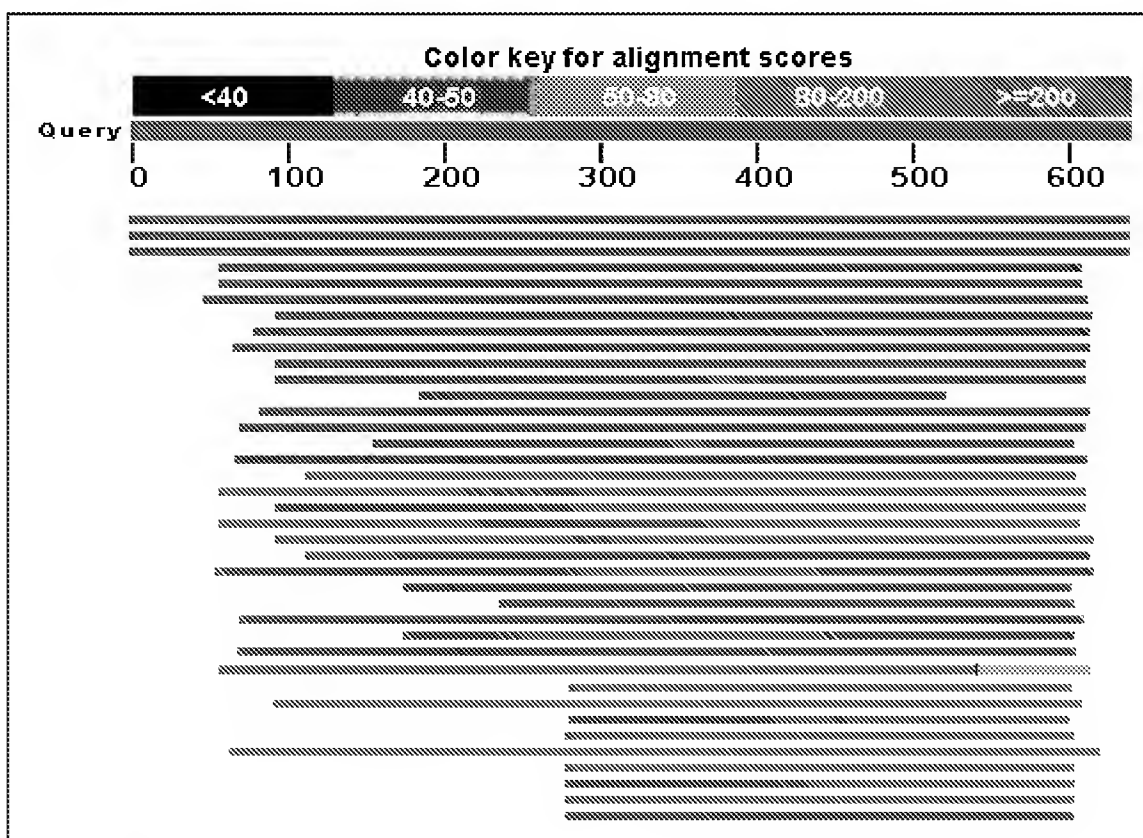
Length adjustment	35
Effective length of query	598
Effective length of database	25209225634
Effective search space	15075116929132
Effective search space used	15075116929132

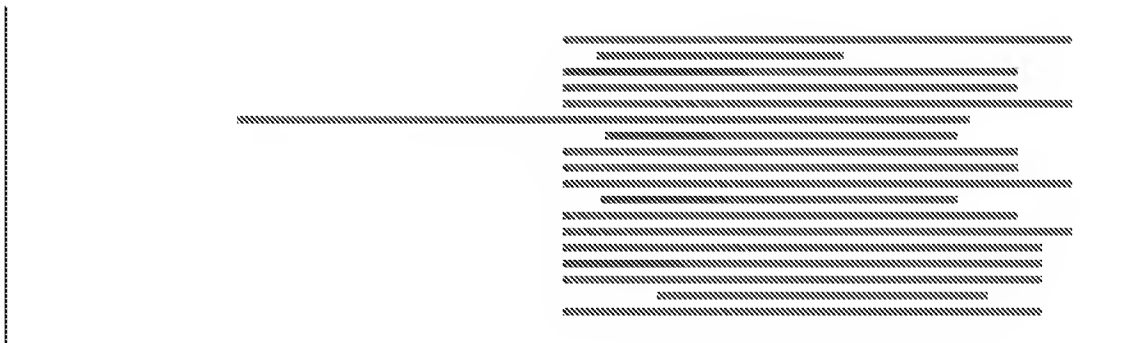
[Graphic Summary](#)

Distribution of 106 Blast Hits on the Query Sequence

?

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

U89363.1	<i>Pseudomonas putida</i> P38K, amidase, nitrile hydratase alpha subunit, nitrile hydratase beta subunit, and P14K genes, complete cds	1142	1142	100%	0.0	100%
AY743666.1	<i>Comamonas testosteroni</i> strain 5-MGAM-4D amidase, nitrile hydratase alpha subunit, nitrile hydratase beta subunit, and P7K genes, complete cds	1063	1063	100%	0.0	97%
AM902716.1	<i>Bordetella petrii</i> strain DSM 12804, complete genome	812	812	100%	0.0	88%
AJ971318.1	<i>Agrobacterium tumefaciens</i> nitrile metabolism operon	349	349	86%	1e-92	74%
AJ511276.1	<i>Agrobacterium tumefaciens</i> NHase-alpha gene for nitrile hydratase alpha subunit and NHase-beta gene for nitrile hydratase beta subunit	349	349	86%	1e-92	74%
CP000964.1	<i>Klebsiella pneumoniae</i> 342, complete genome	300	300	88%	5e-78	71%
CP000250.1	<i>Rhodopseudomonas palustris</i> HaA2, complete genome	262	262	81%	1e-66	71%
CP001001.1	<i>Methylobacterium radiotolerans</i> JCM 2831, complete genome	259	259	83%	1e-65	71%
CP000943.1	<i>Methylobacterium</i> sp. 4-46, complete genome	235	235	85%	2e-58	70%
CP001096.1	<i>Rhodopseudomonas palustris</i> TIE-1, complete genome	219	219	80%	1e-53	69%
BX572602.1	<i>Rhodopseudomonas palustris</i> CGA009 complete genome; segment 10/16	219	219	80%	1e-53	69%
AJ548497.1	<i>Agrobacterium tumefaciens</i> partial nhase gene for nitrile hydratase alpha subunit, strain DSM 9674, 5' end	217	217	52%	4e-53	74%
CP001053.1	<i>Burkholderia phytofirmans</i> PsJN chromosome 2, complete sequence	214	289	83%	5e-52	68%
AL591688.1	<i>Sinorhizobium meliloti</i> 1021 complete chromosome	208	208	84%	2e-50	69%
X64360.1	<i>R. rhodochrous</i> gene for L-NHase	208	208	69%	2e-50	70%
CP000301.1	<i>Rhodopseudomonas palustris</i> BisB18, complete genome	203	203	85%	1e-48	68%
BA000012.4	<i>Mesorhizobium loti</i> MAFF303099 DNA, complete genome	199	199	76%	1e-47	69%
CP000738.1	<i>Sinorhizobium medicae</i> WSM419, complete genome	197	197	86%	4e-47	68%
BA000040.2	<i>Bradyrhizobium japonicum</i> USDA 110 DNA, complete genome	187	187	44%	8e-44	74%
CP000133.1	<i>Rhizobium etli</i> CFN 42, complete genome	183	183	85%	9e-43	68%
CP000494.1	<i>Bradyrhizobium</i> sp. BTA11, complete genome	179	179	81%	1e-41	68%
CU234118.1	<i>Bradyrhizobium</i> sp. ORS278, complete sequence	179	179	78%	1e-41	68%
CP000476.1	<i>Arthrobacter aureus</i> TCl plasmid TC2, complete sequence	178	178	87%	4e-41	67%
CP000283.1	<i>Rhodopseudomonas palustris</i> BisB5, complete genome	174	217	80%	5e-40	80%
EU333001.1	<i>Mesorhizobium</i> sp. F28 insertion sequence IS21, partial sequence; nitrile hydratase beta subunit, nitrile hydratase alpha subunit, and nitrile hydratase beta-like protein genes, complete cds; and unknown genes	167	167	66%	7e-38	69%
AJ306168.1	Uncultured bacterium BD1 partial nha gene for nitrile hydratase alpha chain	163	163	57%	9e-37	69%
CP001191.1	<i>Rhizobium leguminosarum</i> bv. trifolii WSM2304, complete genome	159	159	84%	1e-35	67%
M74531.1	<i>Rhodobacter</i> sp. enantiomer-selective amidase (amdA), nitrile hydratase alpha- and beta-subunit (nthA and nthB) genes, complete cds	156	156	66%	1e-34	68%
AM236080.1	<i>Rhizobium leguminosarum</i> bv. viciae chromosome complete genome, strain 3841	150	150	83%	5e-33	67%
CP000511.1	<i>Mycobacterium vanbaalenii</i> PYR-1, complete genome	149	303	87%	2e-32	81%

AJ306163.1	Uncultured bacterium Prl partial nha gene for nitrile hydratase alpha chain	149	149	50%	2e-32	68%
CT971493.5	Zebrafish DNA sequence from clone RP71-31A12, complete sequence	138	138	80%	3e-29	66%
AJ306164.1	Uncultured bacterium Rcl partial nha gene for nitrile hydratase alpha chain	132	132	49%	1e-27	69%
AY223832.1	Rhodococcus erythropolis ENG-AN033 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	131	131	50%	5e-27	69%
CP000377.1	Silicibacter sp. TM1040, complete genome	127	127	87%	6e-26	65%
AY223831.1	Rhodococcus erythropolis ARG-AN025 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	125	125	50%	2e-25	69%
AY223830.1	Rhodococcus erythropolis ARG-AN024 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	125	125	50%	2e-25	69%
AY223827.1	Rhodococcus erythropolis ANT-AN007 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	125	125	50%	2e-25	69%
AY223825.1	Rhodococcus erythropolis 67-BEN001 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	125	125	50%	2e-25	69%
AB105912.1	Rhodococcus globerulus aldoxime metabolism gene cluster (orfa, oxd, nhr2, nhr1, ami, nha1, nha2, nhr3, orfb), complete cds, strain:A-4	125	125	50%	2e-25	69%
CP000830.1	Dinoroseobacter shibae DFL 12, complete genome	123	123	24%	8e-25	79%
AY223833.1	Rhodococcus erythropolis 871-AN042 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	123	123	45%	8e-25	69%
AY223828.1	Rhodococcus erythropolis IND-AN014 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	123	123	45%	8e-25	69%
AY223834.1	Rhodococcus erythropolis 871-AN053 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	122	122	50%	3e-24	68%
CP001074.1	Rhizobium etli CIAT 652, complete genome	118	118	73%	3e-23	65%
EU573979.1	Streptomyces rimosus toyocamycin/sangivamycin biosynthesis gene cluster, complete sequence	116	116	35%	1e-22	71%
AM946017.1	Rhodococcus erythropolis aldoxime dehydratase, amidase and nitrile hydratase gene cluster (nhr4, oxd, nhr2, nhr1, ami, nha1, nha2, nhr3, ORFb), strain A4	114	114	45%	4e-22	69%
AM710613.1	Rhodococcus erythropolis nha1 gene for nitrile hydratase alpha subunit and nha2 gene for nitrile hydratase beta subunit, strain A4	114	114	45%	4e-22	69%
EU130914.1	Rhodococcus erythropolis nitrile hydratase alpha subunit gene, complete cds	113	113	50%	1e-21	68%
CP000697.1	Acidiphilium cryptum JF-5, complete genome	113	113	35%	1e-21	71%
CP000431.1	Rhodococcus sp. RHA1, complete genome	113	173	45%	1e-21	68%
AY223836.1	Rhodococcus erythropolis DSM13002 nitrile hydratase alpha subunit gene, complete cds; and nitrile hydratase beta subunit gene, partial cds	113	113	50%	1e-21	68%
AJ716149.1	Microbacterium sp. AJ115 ORFA, nhr1 gene, ami gene, nha1 gene, nha2 gene and nha2 gene (partial)	113	113	47%	1e-21	68%
X54074.1	Rhodococcus genes for amidase and nitrile hydratase alpha and beta subunits	111	111	47%	5e-21	68%
AJ278349.1	Rhodococcus sp. AJ270 ami gene (partial), nha gene, nhb gene and ORF4	111	111	47%	5e-21	68%
AJ577856.1	Variovorax sp. DSM 11402 partial nhase gene for putative nitrile hydratase alpha subunit	111	111	33%	5e-21	71%

Z48769.1	Rhodococcus sp. ACV2 partial amdA, nthA and nthB genes	111	111	47%	5e-21	68%
X14668.1	Rhodococcus spec. gene for nitrile hydratase (NHase)	111	111	47%	5e-21	68%
AJ716152.1	Rhodococcus erythropolis oxd gene, ORFA, nhr1 gene, ami gene, nha1 gene, nha2 gene, nha3 gene, ORFE and ORFF (partial), strain AJ270	111	111	47%	5e-21	68%
AJ490527.1	Rhodococcus erythropolis nitrile hydratase-amidase operon (nhr2, nhr1, ami nha, nhb, nh3 and partial ORFE genes)	111	111	47%	5e-21	68%
AB016078.1	Rhodococcus sp. N-771 genes for nitrile hydratase regulator 2 and 1, amidase, nitrile hydratase alpha and beta subunits and nitrile hydratase activator, complete cds	111	111	47%	5e-21	68%
CP000712.1	Pseudomonas putida F1, complete genome	109	109	69%	2e-20	67%
AY223829.1	Rhodococcus erythropolis 870-AN019 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	109	109	45%	2e-20	68%
CP000362.1	Roseobacter denitrificans OCh 114, complete genome	107	107	74%	6e-20	65%
AY223835.1	Rhodococcus erythropolis DSM43006 nitrile hydratase alpha subunit gene, complete cds; and nitrile hydratase beta subunit gene, partial cds	107	107	50%	6e-20	67%
AY223826.1	Rhodococcus erythropolis 122-AN065 nitrile hydratase alpha subunit and nitrile hydratase beta subunit genes, complete cds; and Orf1188 gene, partial cds	107	107	47%	6e-20	68%
M60264.1	Brevibacterium enantiomer-selective amidase (amdA) gene and nitrile hydratase alpha-subunit, complete cds and 5' end	107	107	45%	6e-20	68%
AJ544772.1	Rhodococcus erythropolis partial nhase gene for nitrile hydratase alpha subunit	105	105	33%	2e-19	70%
AJ306167.1	Uncultured bacterium BD2 nha gene for nitrile hydratase alpha chain	104	104	43%	7e-19	69%
AY141130.1	Nocardia sp. JBRs nitrile hydratase beta subunit and nitrile hydratase alpha subunit genes, complete cds	104	104	43%	7e-19	69%
AY168347.1	Nocardia sp. YS-2002 nitrile hydratase beta subunit (NH2) and nitrile hydratase alpha subunit (NH1) genes, complete cds	104	104	43%	7e-19	69%
CP000386.1	Rubrobacter xylanophilus DSM 9941, complete genome	102	102	47%	2e-18	68%
AJ548492.1	Rhodococcus erythropolis partial nhase gene for nitrile hydratase alpha subunit, strain DSM 11397	102	102	31%	2e-18	71%
D14454.1	Rhodococcus erythropolis nitrile hydratase genes	102	102	36%	2e-18	69%
AY654301.1	Rhodococcus rhodochrous nitrile hydratase regulator 1 (nhmC), nitrile hydratase regulator 2 (nhmD), nitrile hydratase beta subunit (nhmB), nitrile hydratase alpha subunit (nhmA), and nitrile hydratase activator (nhmG) genes, complete cds	100	100	43%	9e-18	69%
AB211984.1	Rhodococcus pyridinivorans genes for nitrile hydratase beta subunit, nitrile hydratase alpha subunit, complete cds	100	100	43%	9e-18	69%
AJ548491.1	Rhodococcus erythropolis partial nhase gene for nitrile hydratase alpha subunit, strain DSM 9685	100	100	33%	9e-18	70%
X64359.1	R.rhodochrous gene for H-NHase	100	100	43%	9e-18	69%
X86737.1	Rhodococcus sp. H-NHase gene	100	100	43%	9e-18	69%
AJ582605.1	Rhodococcus pyridinivorans nhhb gene for nitrile hydratase beta subunit and nhha gene for nitrile hydratase alpha subunit	100	100	43%	9e-18	69%
D67027.1	Rhodococcus rhodochrous J1 regulator genes for high-molecular-mass nitrile hydratase, complete cds	100	100	43%	9e-18	69%
AJ306165.1	Uncultured bacterium SP1 partial nha gene for nitrile hydratase alpha chain	98.7	98.7	33%	3e-17	71%
AB007989.1		95.1	95.1	45%	4e-16	67%

	Thiobacillus thioparus scnB, scnA, scnC gene for thiocyanate hydrolase beta, alpha, gamma subunit, complete cds						
DQ073954.1	Herbaspirillum seropedicae strain S31 putative amidase gene, partial cds; and disrupted nitrile hydratase subunit alpha (nha1) gene, partial sequence	93.3	93.3	47%	1e-15	67%	
AJ548494.1	Rhodococcus sp. CCM1 458 partial nhase gene for nitrile hydratase alpha subunit, strain CCM1 458	87.8	87.8	33%	5e-14	69%	
AJ548493.1	Rhodococcus erythropolis partial nhase gene for nitrile hydratase alpha subunit, strain CCM1 1005	87.8	87.8	31%	5e-14	69%	
AB193508.1	Pseudomonas sp. K-9 orfa, oxd, orfc, orfd, ami, nha1, nha2, nhr, orfi, orfj genes for araC/nitR homologue, aldoxime dehydratase, hypothetical protein, myoglobin-like protein, amidase, nitrile hydratase alpha subunit, nitrile hydratase beta subunit, P45K homologue, hypothetical protein, Acyl-CoA ligase, complete cds	87.8	87.8	57%	5e-14	66%	
AJ306169.1	Rhodococcus erythropolis partial nha gene for nitrile hydratase alpha chain, strain JCM3191	86.0	86.0	38%	2e-13	68%	
CP001192.1	Rhizobium leguminosarum bv. trifolii WSM2304 plasmid pRLG201, complete sequence	84.2	84.2	57%	7e-13	64%	
AP009384.1	Azorhizobium caulinodans ORS 571 DNA, complete genome	84.2	84.2	44%	7e-13	66%	
CP000656.1	Mycobacterium gilvum PYR-GCK, complete genome	77.0	77.0	46%	1e-10	66%	
CP000480.1	Mycobacterium smegmatis str. MC2 155, complete genome	77.0	128	49%	1e-10	72%	
CP000954.1	Synechococcus sp. PCC 7002 plasmid pAQ4, complete sequence	73.4	73.4	17%	1e-09	74%	
AB083342.1	Bacillus cereus nha gene for nitrile hydratase alpha-subunit, partia cds, strain: IFO 3466	62.6	62.6	21%	2e-06	69%	
AM236085.1	Rhizobium leguminosarum bv. viciae plasmid pRL11 complete genome, strain 3841	60.8	60.8	35%	8e-06	65%	
CP000580.1	Mycobacterium sp. JLS, complete genome	55.4	55.4	42%	3e-04	64%	
CP000518.1	Mycobacterium sp. KMS, complete genome	55.4	55.4	42%	3e-04	64%	
CP000384.1	Mycobacterium sp. MCS, complete genome	55.4	55.4	42%	3e-04	64%	
CP001027.1	Burkholderia ambifaria MC40-6 chromosome 3, complete sequence	53.6	53.6	8%	0.001	82%	
AB083341.1	Bacillus cereus nha gene for nitrile hydratase alpha-subunit, partia cds, strain:Tim-r01	53.6	53.6	21%	0.001	68%	